

WO 2004/055189

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SEQUENCE LISTING

<110> Akzo Nobel N.V.

<120> New expression system from Rhodococcus

<130>

<140>

<141>

<160> 13

<170> PatentIn-Ver. 2.1

<210> 1

<211> 1543

<212> DNA

<213> Rhodococcus erythropolis

<220>

<221> CDS

<222> (1)..(1533)

<400> 1

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atg cag gac tgg acc agc gag tgc gac gtg ttg gta gtc ggc tcc ggc 48
Met Gln Asp Trp Thr Ser Glu Cys Asp Val Leu Val Val Gly Ser Gly
  1             5             10             15

ggc gga gcg ctg acc ggc gca tat acc gcc gct gct cag gga ttg acg 96
Gly Gly Ala Leu Thr Gly Ala Tyr Thr Ala Ala Ala Gln Gly Leu Thr
          20             25             30

acg atc gtc ctc gag aaa acc gat cgt ttc ggc ggg acc tcc gc c tac 144
Thr Ile Val Leu Glu Lys Thr Asp Arg Phe Gly Gly Thr Ser Ala Tyr
      35             40             45

tcg ggc gcc tcg atc tgg ctc cca ggt acc cag gtg cag gaa cgc gcc 192
Ser Gly Ala Ser Ile Trp Leu Pro Gly Thr Gln Val Gln Glu Arg Ala
  50             55             60

gga ctt ccc gac tcg acc gag aat gcc cgc acc tat ctg cgc gcg ttg 240
Gly Leu Pro Asp Ser Thr Glu Asn Ala Arg Thr Tyr Leu Arg Ala Leu
  65             70             75             80

ctc ggt gac gcc gag tcc gag cgc cag gac gcc tac gtc gag acc gct 288
Leu Gly Asp Ala Glu Ser Glu Arg Gln Asp Ala Tyr Val Glu Thr Ala
          85             90             95

ccc gct gtc gtc gct cta ctc gag cag aac ccg aac atc gaa ttc gag 336
Pro Ala Val Val Ala Leu Leu Glu Gln Asn Pro Asn Ile Glu Phe Glu
      100             105             110

ttc cgt gcg ttc ccc gac tac tac aaa gcc gaa ggc cgg atg gac acg 384
Phe Arg Ala Phe Pro Asp Tyr Lys Ala Glu Gly Arg Met Asp Thr
      115             120             125

gga cgc tcc atc aac cct ctc gat ctc gat ccc gcc gac atc ggt gac 432
Gly Arg Ser Ile Asn Pro Leu Asp Leu Asp Pro Ala Asp I le Gly Asp
      130             135             140

ctc gcc ggc aag gtg cgt ccg gaa ctg gac caa gac cgc acc ggt cag 480
Leu Ala Gly Lys Val Arg Pro Glu Leu Asp Gln Asp Arg Thr Gly Gln
      145             150             155             160

gat cat gct ccc ggc ccg atg atc ggt ggg cgc gca ctg atc ggc cgt 528
Asp His Ala Pro Gly Pro Met Ile Gly Gly Arg Ala Leu Ile Gly Arg
          165             170             175

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ctg ctg gcc gca gtt cag agc acc ggt aag gca gaa ctt cgc acc gaa 576
 Leu Leu Ala Ala Val Gln Ser Thr Gly Lys Ala Glu Leu Arg Thr Glu
 180 185 190

tcc gtc ctc acc tcc ctg atc gtg gaa gac ggc cgt gtt gtc ggc gcc 624
 Ser Val Leu Thr Ser Leu Ile Val Glu Asp Gly Arg Val Val Gly Ala
 195 200 205

gag gtc gaa tcc ggc ggc gaa acc cag cga atc aag gcg aac cgc ggt 672
 Glu Val Glu Ser Gly Gly Glu Thr Gln Arg Ile Lys Ala Asn Arg Gly
 210 215 220

gtc ctg atg gca gca ggc ggc atc gaa ggc aac gcc gag atg cgt gag 720
 Val Leu Met Ala Ala Gly Gly Ile Glu Gly Asn Ala Glu Met Arg Glu
 225 230 235 240

cag gca ggc acc ccc ggc aag gcg atc tgg agt atg ggt ccc ttc ggc 768
 Gln Ala Gly Thr Pro Gly Lys Ala Ile Trp Ser Met Gly Pro Phe Gly
 245 250 255

gcc aac acc ggc gac gcg atc tct gcc ggt att gc t gtc ggc ggc gca 816
 Ala Asn Thr Gly Asp Ala Ile Ser Ala Gly Ile Ala Val Gly Gly Ala
 260 265 270

aca gcc ttg ctc gat cag gcg tgg ttc tgc ccc ggc gtc gag cag ccc 864
 Thr Ala Leu Leu Asp Gln Ala Trp Phe Cys Pro Gly Val Glu Gln Pro
 275 280 285

gac ggc agc gcc gcc ttc atg gtc ggc gtt cgc ggt ggc ctc gtc gtc 912
 Asp Gly Ser Ala Ala Phe Met Val Gly Val Arg Gly Gly Leu Val Val
 290 295 300

gac agc gcc ggt gag gcg tac ctc aac gag tgc ctt ccg tac gac cag 960
 Asp Ser Ala Gly Glu Arg Tyr Leu Asn Glu Ser Leu Pro Tyr Asp Gln
 305 310 315 320

ttc gga cga gcc atg gat gct cac gac gac aac ggt tct gcc gtg ccg 1008
 Phe Gly Arg Ala Met Asp Ala His Asp Asn Gly Ser Ala Val Pro
 325 330 335

tgc ttc atg atc ttc gac tgc gcg gag ggt ggc gga ctg ccc gcc atc 1056
 Ser Phe Met Ile Phe Asp Ser Arg Glu Gly Gly Gly Leu Pro Ala Ile
 340 345 350

tgc atc ccg aac acg gcg ccc gcc aag cac ctc gaa gcc gga acg tgg 1104
 Cys Ile Pro Asn Thr Ala Pro Ala Lys His L eu Glu Ala Gly Thr Trp
 355 360 365

gtc ggt gcc gac act ctc gaa gaa ctc gct gcc aag acc gga cta ccg 1152
 Val Gly Ala Asp Thr Leu Glu Glu Leu Ala Ala Lys Thr Gly Leu Pro
 370 375 380

gcc gac gca ttg cgc agc act gtc gaa aag ttc aac gat gcc gca aaa 1200
 Ala Asp Ala Leu Arg Ser Thr Val Glu Lys Phe Asn Asp Ala Ala Lys
 385 390 395 400

ctg ggc gtc gac gaa gag ttc cat cgc ggc gaa gac ccg tac gac gcg 1248
 Leu Gly Val Asp Glu Glu Phe His Arg Gly Glu Asp Pro Tyr Asp Ala
 405 410 415

ttc ttc tgc cca ccc aac ggc ggt gcg aat gcg gca ctg acg gcc atc 1296
 Phe Phe Cys Pro Pro Asn Gly Gly Ala Asn Ala Ala Leu Thr Ala Ile
 420 425 430

gag aac gga ccg ttc tac gcg gcc gcg atc gtc ctc agt gac ctc ggc 1344
 Glu Asn Gly Pro Phe Tyr Ala Ala Arg Ile Val Leu Ser Asp Leu Gly

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      435              440              445
acc aag ggc gga ttg gtc acc gac gtc aac ggc cga gtc ctg cgt gct 1392
Thr Lys Gly Gly Leu Val Thr Asp Val Asn Gly Arg Val Leu Arg Ala
   450              455              460

gac ggc agc gcc atc gac ggc ctg tac gcc gcc ggc aac acg agc gcg 1440
Asp Gly Ser Ala Ile Asp Gly Leu Tyr Ala Ala Gly Asn Thr Ser Ala
   465              470              475              480

tca ctg agc ggc cgc ttc tac ccc gcc ccc gga gtt cca ctc ggc acg 1488
Ser Leu Ser Gly Arg Phe Tyr Pro Gly Pro Gly Val Pro Leu Gly Thr
   485              490              495

gct atg gtc ttc tcg tac cga gca gct cag gac atg gcg aag taa 1533
Ala Met Val Phe Ser Tyr Arg Ala Ala Gln Asp Met Ala Lys
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cgcagttcaa 1543

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<210> 2
<211> 511
<212> PRT
<213> Rhodococcus erythropolis

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Gly Gly Ala Leu Thr Gly Ala Tyr Thr Ala Ala Ala Gln Gly Leu Thr
   20              25              30

Thr Ile Val Leu Glu Lys Thr Asp Arg Phe Gly Gly Thr Ser Ala Tyr
   35              40              45

Ser Gly Ala Ser Ile Trp Leu Pro Gly Thr Gln Val Gln Glu Arg Ala
   50              55              60

Gly Leu Pro Asp Ser Thr Glu Asn Ala Arg Thr Tyr Leu Arg Ala Leu
   65              70              75              80

Leu Gly Asp Ala Glu Ser Glu Arg Gln Asp Ala Tyr Val Glu Thr Ala
   85              90              95

Pro Ala Val Val Ala Leu Leu Glu Gln Asn Pro Asn Ile Glu Phe Glu
  100              105              110

Phe Arg Ala Phe Pro Asp Tyr Tyr Lys Ala Glu Gly Arg Met Asp Thr
  115              120              125

Gly Arg Ser Ile Asn Pro Leu Asp Leu Asp Pro Ala Asp Ile Gly Asp
  130              135              140

Leu Ala Gly Lys Val Arg Pro Glu Leu Asp Gln Asp Arg Thr Gly Gln
  145              150              155              160

Asp His Ala Pro Gly Pro Met Ile Gly Gly Arg Ala Leu Ile Gly Arg
  165              170              175

Leu Leu Ala Ala Val Gln Ser Thr Gly Lys Ala Glu Leu Arg Thr Glu
  180              185              190

Ser Val Leu Thr Ser Leu Ile Val Glu Asp Gly Arg Val Val Gly Ala
  195              200              205

Glu Val Glu Ser Gly Gly Glu Thr Gln Arg Ile Lys Ala Asn Arg Gly

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210 215 220
 Val Leu Met Ala Ala Gly Gly Ile Glu Gly Asn Ala Glu Met Arg Glu
 225 230 235 240
 Gln Ala Gly Thr Pro Gly Lys Ala Ile Trp Ser Met Gly Pro Phe Gly
 245 250 255
 Ala Asn Thr Gly Asp Ala Ile Ser Ala Gly Ile Ala Val Gly Gly Ala
 260 265 270
 Thr Ala Leu Leu Asp Gln Ala Trp Phe Cys Pro Gly Val Glu Gln Pro
 275 280 285
 Asp Gly Ser Ala Ala Phe Met Val Gly Val Arg Gly Gly Leu Val Val
 290 295 300
 Asp Ser Ala Gly Glu Arg Tyr Leu Asn Glu Ser Leu Pro Tyr Asp Gln
 305 310 315 320
 Phe Gly Arg Ala Met Asp Ala His Asp Asp Asn Gly Ser Ala Val Pro
 325 330 335
 Ser Phe Met Ile Phe Asp Ser Arg Glu Gly Gly Gly Leu Pro Ala Ile
 340 345 350
 Cys Ile Pro Asn Thr Ala Pro Ala Lys His Leu Glu Ala Gly Thr Trp
 355 360 365
 Val Gly Ala Asp Thr Leu Glu Glu Leu Ala Ala Lys Thr Gly Leu Pro
 370 375 380
 Ala Asp Ala Leu Arg Ser Thr Val Glu Lys Phe Asn Asp Ala Ala Lys
 385 390 395 400
 Leu Gly Val Asp Glu Glu Phe His Arg Gly Glu Asp Pro Tyr Asp Ala
 405 410 415
 Phe Phe Cys Pro Pro Asn Gly Gly Ala Asn Ala Ala Leu Thr Ala Ile
 420 425 430
 Glu Asn Gly Pro Phe Tyr Ala Ala Arg Ile Val Leu Ser Asp Leu Gly
 435 440 445
 Thr Lys Gly Gly Leu Val Thr Asp Val Asn Gly Arg Val Leu Arg Ala
 450 455 460
 Asp Gly Ser Ala Ile Asp Gly Leu Tyr Ala Ala Gly Asn Thr Ser Ala
 465 470 475 480
 Ser Leu Ser Gly Arg Phe Tyr Pro Gly Pro Gly Val Pro Leu Gly Thr
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 Ala Met Val Phe Ser Tyr Arg Ala Ala Gln Asp Met Ala Lys
 500 505 510

<210> 3
 <211> 158
 <212> DNA
 <213> Rhodococcus erythropolis

<400> 3
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 atctcggcat attgcccgt cagtgggacc tggcatggcc ttccagtgcc gtgcgggtatt 120

ccgtggacac cccaccctct tggagtaagg acgcaatg 158

<210> 4
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 4
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<210> 5
<211> 624
<212> DNA
<213> Rhodococcus erythropolis

<220>
<221> CDS
<222> (1)..(624)

<400> 5
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1 5 10 15
ccc agt tcg gac gag cag cgg gcg cgc cat gtg cgg atg ctg gaa gcg 96
Pro Ser Ser Asp Glu Gln Arg Ala Arg His Val Arg Met Leu Glu Ala
20 25 30
gcc gcc gaa ttg ggg acc gag aaa gaa ctc tca cgg gtt cag atg cac 144
Ala Ala Glu Leu Gly Thr Glu Lys Glu Leu Ser Arg Val Gln Met Hi s
35 40 45
gaa gtt gcc aag cgg gca ggc gtg gcc atc ggc act ctc tac cgc tat 192
Glu Val Ala Lys Arg Ala Gly Val Ala Ile Gly Thr Leu Tyr Arg Tyr
50 55 60
ttc cct tcg aag acg cac ctc ttc gtc gct gtg atg gtc gag cag atc 240
Phe Pro Ser Lys Thr His Leu Phe Val Ala Val Met Val Glu Gln Ile
65 70 75 80
gat cag atc ggc gac agt ttc gcc aag cat c ag gtg cag tcg gcc aat 288
Asp Gln Ile Gly Asp Ser Phe Ala Lys His Gln Val Gln Ser Ala Asn
85 90 95
ccg cag gac gcc gtg tac gag gtc ctg gtg cgc gcg act cgc ggg tta 336
Pro Gln Asp Ala Val Tyr Glu Val Leu Val Arg Ala Thr Arg Gly Leu
100 105 110
ctg cgt cgg ccg gcc ctt tcg act gog atg ctg cag tcg tcc agt acc 384
Leu Arg Arg Pro Ala Leu Ser Thr Ala Met Leu Gln Ser Ser Ser Thr
115 120 125
gcc aac gtc gcg acg gtg ccg gac gtg ggc aag atc gat cgc ggc ttc 432
Ala Asn Val Ala Thr Val Pro Asp Val Gly Lys Ile Asp Arg Gly Phe
130 135 140
cgg cag atc atc ctc gat gcg gcc ggg atc gag aac ccg acc gag gaa 480
Arg Gln Ile Ile Leu Asp Ala Ala Gly Ile Glu Asn Pro Thr Glu Glu
145 150 155 160
gac aac acc ggg ttg cgt ctg ctg atg cag ctg tgg ttc ggg gtc atc 528
Asp Asn Thr Gly Leu Arg Leu Leu Met Gln Leu Trp Phe Gly Val Ile

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                165                170                175
caa tgc tgc ctc aac ggt cga att tcc atc ccg gat gcg gag tac gac 576
Gln Ser Cys Leu Asn Gly Arg Ile Ser Ile Pro Asp Ala Glu Tyr Asp
                180                185                190

atc cgc aag ggg tgc gac ctg ctt ctg gtg aat ctc tca cga cac tga 624
Ile Arg Lys Gly Cys Asp Leu Leu Leu Val Asn Leu Ser Arg His
                195                200                205

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<210> 6
 <211> 208
 <212> PRT
 <213> Rhodococcus erythropolis

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<400> 6
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 1          5          10          15

Pro Ser Ser Asp Glu Gln Arg Ala Arg His Val Arg Met Leu Glu Ala
          20          25          30

Ala Ala Glu Leu Gly Thr Glu Lys Glu Leu Ser Arg Val Gln Met His
          35          40          45

Glu Val Ala Lys Arg Ala Gly Val Ala Ile Gly Thr Leu Tyr Arg Tyr
          50          55          60

Phe Pro Ser Lys Thr His Leu Phe Val Ala Val Met Val Glu Gln Ile
          65          70          75          80

Asp Gln Ile Gly Asp Ser Phe Ala Lys His Gln Val Gln Ser Ala Asn
          85          90          95

Pro Gln Asp Ala Val Tyr Glu Val Leu Val Arg Ala Thr Arg Gly Leu
          100          105          110

Leu Arg Arg Pro Ala Leu Ser Thr Ala Met Leu Gln Ser Ser Ser Thr
          115          120          125

Ala Asn Val Ala Thr Val Pro Asp Val Gly Lys Ile Asp Arg Gly Phe
          130          135          140

Arg Gln Ile Ile Leu Asp Ala Ala Gly Ile Glu Asn Pro Thr Glu Glu
          145          150          155          160

Asp Asn Thr Gly Leu Arg Leu Leu Met Gln Leu Trp Phe Gly Val Ile
          165          170          175

Gln Ser Cys Leu Asn Gly Arg Ile Ser Ile Pro Asp Ala Glu Tyr Asp
          180          185          190

Ile Arg Lys Gly Cys Asp Leu Leu Leu Val Asn Leu Ser Arg His
          195          200          205

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<210> 7
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:primer

<400> 7
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<210> 8
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 8
ataaagctta tcgattatgt gtcccgccg cgaac 35

<210> 9
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 9
ataggtacca tatgtgcgtc cttactccaa gaggg 35

<210> 10
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 10
gcgcatatgg ctaagaatca ggcaccc 27

<210> 11
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 11
gcgggatccc tactttctctg ctgcgtgatg 30

<210> 12
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 12
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<210> 13
<211> 30
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 13

gccactagtt cactgcgctg ctctgcacg

30